

Sequence Range: 1 to 6200

10	20	30	40	50	60	70
*	*	*	*	*	*	*
GACGGATCGG	GAGATCTCCC	GATCCCCTAT	GGTCGACTCT	CAGTACAATC	TGCTCTGATG	CCGCATAAGTT
80	90	100	110	120	130	140
*	*	*	*	*	*	*
AAGCCAGTAT	CTGCTCCCTG	CTTGTGTGTT	GGAGGGTCGCT	GAGTAGTGCG	CGAGCAAAAT	TTAGCTACAA
150	160	170	180	190	200	210
*	*	*	*	*	*	*
ACAAGGCAAG	GCTTGACCGA	CAATTGCATG	AAGAACCTGC	TTAGGGTTAG	GCGTTTGCG	CTGCTTCGCG
220	230	240	250	260	270	280
*	*	*	*	*	*	*
ATGTACGGGC	CAGATATACG	CGTTGACATT	GATTATTGAC	TAGTTATTAA	TAGTAATCAA	TTACGGGGTC
290	300	310	320	330	340	350
*	*	*	*	*	*	*
ATTAGTTCAT	AGCCCATATA	TGGAGTTCCG	CGTTACATAA	CTTACGGTAA	ATGGCCCGCC	TGGCTGACCG
360	370	380	390	400	410	420
*	*	*	*	*	*	*
CCCAACGACC	CCCGCCCAT	GACGTCAATA	ATGACGTATG	TTCCCATAGT	AACGCCAATA	GGGACTTTCC
430	440	450	460	470	480	490
*	*	*	*	*	*	*
ATTGACGTCA	ATGGGTGGAC	TATTTACGGT	AAACTGCCA	CTTGGCAGTA	CATCAAGTGT	ATCATATGCC
500	510	520	530	540	550	560
*	*	*	*	*	*	*
AAGTACGCC	CCTATTGACG	TCAATGACGG	TAAATGGCCC	CCCTGGCATT	ATGCCCAAGTA	CATGACCTTA
570	580	590	600	610	620	630
*	*	*	*	*	*	*
TGGGACTTT	CTACTTGGCA	GTACATCTAC	GTATTTGTCA	TCGCTATTAC	CATGGTGATG	CGGTTTGCG
640	650	660	670	680	690	700
*	*	*	*	*	*	*
AGTACATCAA	TGGGCGTGG	TAGCGGTTTG	ACTCACGGGG	ATTTCCAAGT	CTCCACCCCCA	TTGACGTCAA
710	720	730	740	750	760	770
*	*	*	*	*	*	*
TGGGAGTTTG	TTTTGGCACC	AAAATCAACG	GGACTTTCCA	AAATGTGCTA	ACAACCTCCGC	CCCATTGACG
780	790	800	810	820	830	840
*	*	*	*	*	*	*
CAAATGGGCG	GTAGGGGTGT	ACGGTGGGAG	GTCTATATAA	GCAGAGCTCT	CTGGCTAACT	AGAGAACCCA
850	860	870	880	890	900	910
*	*	*	*	*	*	*
CTGCTTAACT	GGCTTATCGA	ATTAATACG	ACTCACTATA	GGGAGACCC	AGCTTCGCAG	AATTCTGCG
920	930	940	950	960	970	980
*	*	*	*	*	*	*
GCTGCTACAG	TGTGTCCAGC	GTCCTGCCTG	GCTGTGCTGA	GUGCTGGAAC	AGTGGCGCAT	CATTCAAGTG
990	1000	1010	1020	1030	1040	1050
*	*	*	*	*	*	*
CACAGTTACC	CATCCTGAGT	CTGGCACCTT	AACTGGCACA	ATTGCCAAAG	TCACAGGTGA	GCTCAGATGC

FIGURE 1

Homo sapiens

1060 1070 1080 1090 1100 1110 1120

* * * * *

ATACCAGGAC ATTGTATGAC GTTCCCTGCT CACATGCCTG CTTTCTTCCT ATAATACAGA TGCTCAACTA

1130 1140 1150 1160 1170 1180 1190

* * * * *

ACTGCTCATG TCCTTATATC ACAGAGGGAA ATTGGAGCTA TCTGAGGAAC TGCCCAGAAG GGAAGGGCAG

1200 1210 1220 1230 1240 1250 1260

* * * * *

AGGGGTCTTG CTCTCCTTGT CTGAGCCATA ACTCTTCTTT CTACCTTCCA GTGAACACCT TCCCACCCCCA

1270 1280 1290 1300 1310 1320 1330

* * * * *

GGTCCACCTG CTACCGCCGC CGTCGGAGGA GCTGGCCCTG AATGAGCTCT TGTCCCTGAC ATGCCCTGGTG

1340 1350 1360 1370 1380 1390 1400

* * * * *

CGAGCTTCA ACCCTAAAGA AGTGCTGGTG CGATGGCTGC ATGGAAATGA GGAGCTGTCC CCAGAAAGCT

1410 1420 1430 1440 1450 1460 1470

* * * * *

ACCTAGTGTG TGAGCCCCTA AAGGAGCCAG GCGAGGGAGC CACCACCTAC CTGGTGACAA GEGTGTGCG

1480 1490 1500 1510 1520 1530 1540

* * * * *

TGTATCAGCT GAAAGCTTGA TATCGAATTG CGGAGGGCGGA ACCGGCAGTG CAGCCCCAAG CCCCGCAGTC

1550 1560 1570 1580 1590

* * * * *

CCCGAGCACG CGTGGCC ATG CGT CCC CTG CGC CCC CGC GCC GCG CTG CTG GCG CTC CTG
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu>
a a a a a ORF RF[1] a a a a a >

1600 1610 1620 1630 1640 1650

* * * * *

GCC TCG CTC CTG GCC GCG CCC CCG GTG GCC CCG GCC GAG GCC CCG CAC CTG GTG CAT
Ala Ser Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val His>
a >

1660 1670 1680 1690 1700 1710

* * * * *

GTG GAC GCG GCC CGC GCG CTG TGG CCC CTG CGG CGC TTC TGG AGG AGC ACA GGC TTC
Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe>
a >

1720 1730 1740 1750 1760 1770

* * * * *

TGC CCC CCG CTG CCA CAC AGC CAG GCT GAC CAG TAC GTC CTC AGC TGG GAC CAG CAG
Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln>
a >

1780 1790 1800 1810 1820

* * * * *

CTC AAC CTC GCC TAT GTG GGC GCC GTC CCT CAC CGC GGC ATC AAG CAG GTC CGG ACC
Leu Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr>
a >

1830 1840 1850 1860 1870 1880

* * * * *

CAC TGG CTG CTG GAG CTT GTC ACC ACC AGG GGG TCC ACT GGA CGG GGC CTG AGC TAC
His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr>

FIGURE 1A

FIGURE 1B

114304

2460	2470	2480	2490	2500	2510
*	*	*	*	*	*
GCG GAC CCG CTG GTG GGC TGG TCC CTG CCA CAG CCG TGG AGG GCG GAC GTG ACC TAC	Ala Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr>				
_____a_____a_____a_____a_____a_____ORF RF[1] _____a_____a_____a_____a_____a_____a_____a_____>					
2520	2530	2540	2550	2560	
*	*	*	*	*	*
GCG GCC ATG GTG GTG AAG GTC ATC GCG CAG CAT CAG AAC CTG CTA CTG GCC AAC ACC	Ala Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Ala Asn Thr>				
_____a_____a_____a_____a_____a_____ORF RF[1] _____a_____a_____a_____a_____a_____a_____a_____>					
2570	2580	2590	2600	2610	2620
*	*	*	*	*	*
ACC TCC GCC TTC CCC TAC GCG CTC CTG AGC AAC GAC AAT GCC TTC CTG AGC TAC CAC	Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His>				
_____a_____a_____a_____a_____a_____ORF RF[1] _____a_____a_____a_____a_____a_____a_____a_____>					
2630	2640	2650	2660	2670	2680
*	*	*	*	*	*
CCG CAC CCC TTC GCG CAG CGC ACG CTC ACC GCG CGC TTC CAG GTC AAC AAC ACC CGC	Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg>				
_____a_____a_____a_____a_____a_____ORF RF[1] _____a_____a_____a_____a_____a_____a_____a_____>					
2690	2700	2710	2720	2730	
*	*	*	*	*	*
CCG CCG CAC GTG CAG CTG TTG CGC AAG CCG GTG CTC ACG GCC ATG GGG CTG CTG GCG	Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala>				
_____a_____a_____a_____a_____a_____ORF RF[1] _____a_____a_____a_____a_____a_____a_____a_____>					
2740	2750	2760	2770	2780	2790
*	*	*	*	*	*
CTG CTG GAT GAG GAG CAG CTC TGG GCC GAA GTG TCG CGG GCC GGG ACC GTC CTG GAC	Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp>				
_____a_____a_____a_____a_____a_____ORF RF[1] _____a_____a_____a_____a_____a_____a_____a_____>					
2800	2810	2820	2830	2840	2850
*	*	*	*	*	*
AGC AAC CAC ACG GTG GGC GTC CTG GCC AGC GCC CAC CGC CCC CAG GGC CCG GCC GAC	Ser Asp His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp>				
_____a_____a_____a_____a_____a_____ORF RF[1] _____a_____a_____a_____a_____a_____a_____a_____>					
2860	2870	2880	2890	2900	2910
*	*	*	*	*	*
GCC TGG CGC GCC GCG GTG CTG ATC TAC GCG AGC GAC ACC CGC GCC CAC CCC AAC	Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn>				
_____a_____a_____a_____a_____a_____ORF RF[1] _____a_____a_____a_____a_____a_____a_____a_____>					
2920	2930	2940	2950	2960	
*	*	*	*	*	*
CGC AGC GTC GCG GTG ACC CTG CGG CTG CGC GGG GTG CCC CCC GGC CCG CGC CTG GTC	Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu Val>				
_____a_____a_____a_____a_____a_____ORF RF[1] _____a_____a_____a_____a_____a_____a_____a_____>					
2970	2980	2990	3000	3010	3020
*	*	*	*	*	*
TAC GTC ACG CGC TAC CTG GAC AAC GGG CTC TGC AGC CCC GAC GGC GAG TGG CGG CGC	Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg Arg>				
_____a_____a_____a_____a_____a_____ORF RF[1] _____a_____a_____a_____a_____a_____a_____a_____>					
3030	3040	3050	3060	3070	3080
*	*	*	*	*	*

FIGURE 1C

CTG GGC CGG CCC GTC TTC CCC ACG GCA GAG CAG TTC CGG CGC ATG CGC GCG GCT GAG
Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Glu Phe Arg Arg Met Arg Ala Ala Glu

a a a a a a ORF RF[1] a a a a a a a a >

3090 **3100** **3110** **3120** **3130**

GAC CCG GTG GCC GCG GCG CCC CGC CCC TTA CCC GCC GGC GGC CGC CTG ACC CTG CGC
Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg>
_ a _ a _ a _ a _ a _ a _ ORF RF[1] _ a _ >

3140 **3150** **3160** **3170** **3180** **3190**

3200 **3210** **3220** **3230** **3240** **3250**

CCG CCC GGG CAG GTC ACG CGG CTC CGC GCC CTG CCC CTG ACC CAA GGG CAG CTG GTT
 Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln Leu Val>
 a a a a a a a a ORF RF[1] a a a a a a a a a a a a >

3260 **3270** **3280** **3290** **3300**

CTG GTC TGG TCG GAT GAA CAC GTG GGC TCC AAG TGC CTG TGG ACA TAC GAG ATC CAG
 Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr Tyr Glu Ile Gln>
 a a a a a a a a ORF RF[1] a a a a a a a a a a a a >

3310 **3320** **3330** **3340** **3350** **3360**

TTC TCT CAG GAC GGT AAG GCG TAC ACC CCG GTC AGC AGG AAG CCA TCG ACC TTC AAC
 Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn>
 a a a a a a ORF RF[1] a a a a a a a a >

3370 **3380** **3390** **3400** **3410** **3420**

CTC TTT GTG TTC AGC CCA GAC ACA GGT GCT GTC TCT GGC TCC TAC CGA GTT CGA GCC
 Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala>
 a a a a a a a ORF RF[1] a a a a a a a a a >

3430 **3440** **3450** **3460** **3470** **3480**

CTG GAC TAC TGG GCC CGA CCA GGC CCC TTC TCG GAC CCT GTG CCG TAC CTG GAG GTC
Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val>
a a a a a a a ORF RF[1] a a a a a a a a a >

3490 **3500** **3510** **3520** **3530** **3540**

* * * * * CCT GTG CCA AGA GGG CCC CCA TCC CCG GGC AAT CCA TGAG CCTGTGCTGA GCCCCCAGTGG
Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro>
 a a a a a a >

3550 3560 3570 3580 3590 3600 3610

3620 3630 3640 3650 3660 3670 3680

TGCAATATAT TTTTATATTT TAAAGGGAAA AAAAAAAGGGG AAAAAAAGGGG AAAAAAAGGGG

3690 **3700** **3710** **3720** **3730** **3740** **3750**

FIGURE 1D

AAAAAAAGGAA AAAAAAAAAG AATTCCCTGCA GCCCGGGGGA TCCACTAGTT CTAGAGGGCC CGTTTAAACC
 *
 3760 3770 3780 3790 3800 3810 3820
 CGCTGATCAG CCTCGACTGT GCCTCTAGT TGCCAGCCAT CTGTTGTTG CCCCTCCCCC GTGCCTTCCT
 *
 3830 3840 3850 3860 3870 3880 3890
 TGACCCCTGGA AGGTGCCACT CCCACTGTCC TTTCTTAATA AAATGAGGAA ATTGCATCGC ATTGTCTGAG
 *
 3900 3910 3920 3930 3940 3950 3960
 TAGGTGTCAT TCTATTCTGG GGGGTGGGGT GGGGCAGGAC AGCAAGGGGG AGGATTGGGA AGACATAGC
 *
 AGGCATGCTG GGGATGCGGT GGGCTCTATG GCTTCTGAGG CGGAAAGAAC CAGCTGGGC TCGAGAGCTT
 *
 3970 3980 3990 4000 4010 4020 4030
 AGGCATGCTG GGGATGCGGT GGGCTCTATG GCTTCTGAGG CGGAAAGAAC CAGCTGGGC TCGAGAGCTT
 *
 4040 4050 4060 4070 4080 4090 4100
 GCGGTAATCA TGGTCATAGC TGTTCCTGT GTGAAATTGT TATCCGCTCA CAATTCCACA CAACATACGA
 *
 4110 4120 4130 4140 4150 4160 4170
 GCCCGGAAGCA TAAAGTGTAA AGCCTGGGGT GCCTAATGAG TGAGCTAACT CACATTAATT GCGTTGCGCT
 *
 4180 4190 4200 4210 4220 4230 4240
 CACTGCCCGC TTTCCAGTCG GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG
 *
 4250 4260 4270 4280 4290 4300 4310
 AGGCCTTTG CGTATTGGGC GCTCTTCCGC TTCCCTCGTC ACTGACTCGC TGCGCTCGGT CGTTGGCTG
 *
 4320 4330 4340 4350 4360 4370 4380
 CGCGGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGGCAGGAA
 *
 4390 4400 4410 4420 4430 4440 4450
 AGAACATGTG AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAAGGCC GCGTTGCTGG CGTTTTCCA
 *
 4460 4470 4480 4490 4500 4510 4520
 TAGGCTCCGC CCCCTGACG AGCATCACAA AAATGACGC TCAAGTCAGA GGTGGCGAAA CCCGACAGGA
 *
 4530 4540 4550 4560 4570 4580 4590
 CTATAAAGAT ACCAGGC GTT TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA
 *
 4600 4610 4620 4630 4640 4650 4660
 CCGGATACCT GTCCGCCTTT CTCCCTCGG GAAGCGTGGC GCTTCTCAA TGCTCACGCT GTAGGTATCT
 *
 4670 4680 4690 4700 4710 4720 4730
 CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT GGGCTGTGTG CACGAACCCC CCGTCAGCC CGACCGCTGC
 *
 4740 4750 4760 4770 4780 4790 4800
 GCCTTATCCG GTAATATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATCGCCACTG GCAGCAGCCA

FIGURE 1E

4810 4820 4830 4840 4850 4860 4870
 * * * * * * *
 CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA

 4880 4890 4900 4910 4920 4930 4940
 * * * * * * *
 CGGCTACACT AGAAGGACAG TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAAGAGTT

 4950 4960 4970 4980 4990 5000 5010
 * * * * * * *
 GGTAGCTCTT GATCCGGCAA ACAAAACCACC GCTGGTAGCG GTGGTTTTTG TGTTTGCAAG CAGCAGATT

 5020 5030 5040 5050 5060 5070 5080
 * * * * * * *
 CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA

 5090 5100 5110 5120 5130 5140 5150
 * * * * * * *
 AAACTCACGT TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTTAAATTAA

 5160 5170 5180 5190 5200 5210 5220
 * * * * * * *
 AAATGAAGTT TTAATCAAT CTAAAGTATA TATGAGTAAA CTTGGTCTGA CAGTTACCAA TGCTTAATCA

 5230 5240 5250 5260 5270 5280 5290
 * * * * * * *
 GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTCATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT

 5300 5310 5320 5330 5340 5350 5360
 * * * * * * *
 AACTACGATA CGGGAGGGCT TACCATCTGG CCCCAGTGCT GCAATGATAC CGCGAGACCC ACGCTCACCG

 5370 5380 5390 5400 5410 5420 5430
 * * * * * * *
 GCTCCAGATT TATCAGCAAT AAACCCAGCCA GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT

 5440 5450 5460 5470 5480 5490 5500
 * * * * * * *
 CCGCCTCCAT CCAGTCTATT AATTGTTGCC GGGAGCTAG AGTAAGTAGT TCGCCAGTTA ATAGTTTGC

 5510 5520 5530 5540 5550 5560 5570
 * * * * * * *
 CAACGTTGTT GCCATTGCTA CAGGCATCGT GGTGTCACGC TCGTCGTTG GTATGGCTTC ATTCAAGCTCC

 5580 5590 5600 5610 5620 5630 5640
 * * * * * * *
 CGTTCCCAAC GATCAAGGCG AGTTACATGA TCCCCCATGT TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC

 5650 5660 5670 5680 5690 5700 5710
 * * * * * * *
 CTCCGATCGT TGTCAGAACT AAGTTGGCCG CAGTGTATC ACTCATGGTT ATGGCAGCAC TGCATARTTC

 5720 5730 5740 5750 5760 5770 5780
 * * * * * * *
 TCTTACTGTC ATGCCATCCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA

 5790 5800 5810 5820 5830 5840 5850
 * * * * * * *
 TAGTGTATGC GGCGACCGAG TTGCTCTTGC CCGCGTCAA TACGGGATAA TACCGCGCCA CATAGCAGAA

 5860 5870 5880 5890 5900 5910 5920
 * * * * * * *

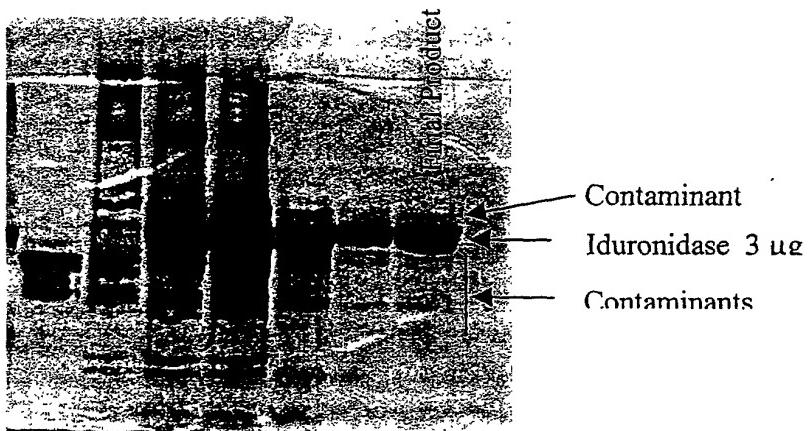
FIGURE 1F

CTTTAAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG AAAACTCTCA AGGATCTTAC CGCTGTTGAG
5930 5940 5950 5960 5970 5980 5990
* * * * * * * * * * * * * * * *
ATCCAGTTCG ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTCAC CAGCGTTCT
6000 6010 6020 6030 6040 6050 6060
* * * * * * * * * * * * * * * *
GGGTGAGCAA AACAGGAAG GCAAAATGCC GCAAAAAAGG GAATAAGGGC GACACGGAAA TGTTGAATAC
6070 6080 6090 6100 6110 6120 6130
* * * * * * * * * * * * * * * *
TCATACTCTT CCTTTTCAA TATTATTGAA GCATTTATCA GGGTTATTGT CTCATGACCG GATACATATT
6140 6150 6160 6170 6180 6190 6200
* * * * * * * * * * * * * * * *

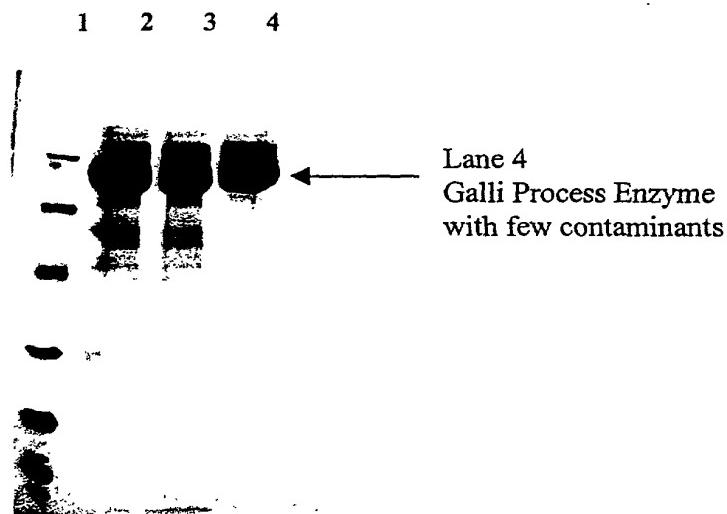
FIGURE 1G

FIGURE 2. SDS-POLYACRYLAMIDE GELS DEMONSTRATING IMPROVEMENTS IN PURITY

Gel using the Kakkis et al 1994, published procedure for purification



Gel using the new Galli Process contained in this application



1. Molecular Weight Marker
2. Prior Process Carson (nonpublished) Batch 2000C9001 Reference Reduced (7.5 μ g)
3. Same Batch 2000C9001 Reference Reduced (5.0 μ g)
4. Galli Process Enzyme Batch P10006 (5.0 μ g)

FIGURE 2

FIGURE 3A IDURONIDASE PRODUCTION USING THE GALLI PROCESS

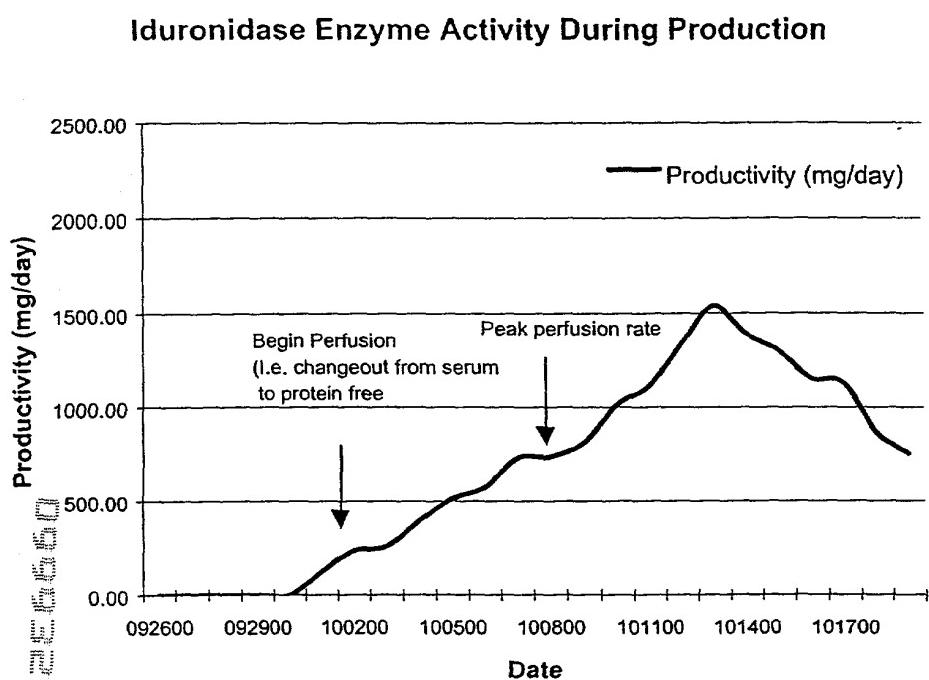
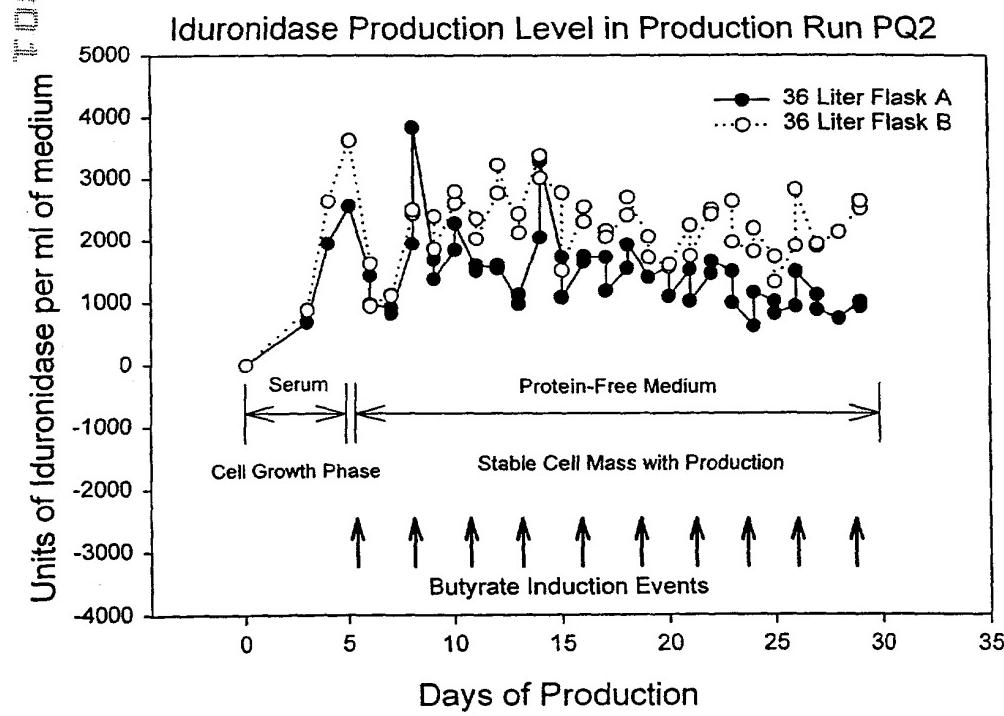


FIGURE 3B. IDURONIDASE PRODUCTION USING BUTYRATE INDUCTION



Reduction in Liver Volume During Enzyme Therapy

FIGURE 4

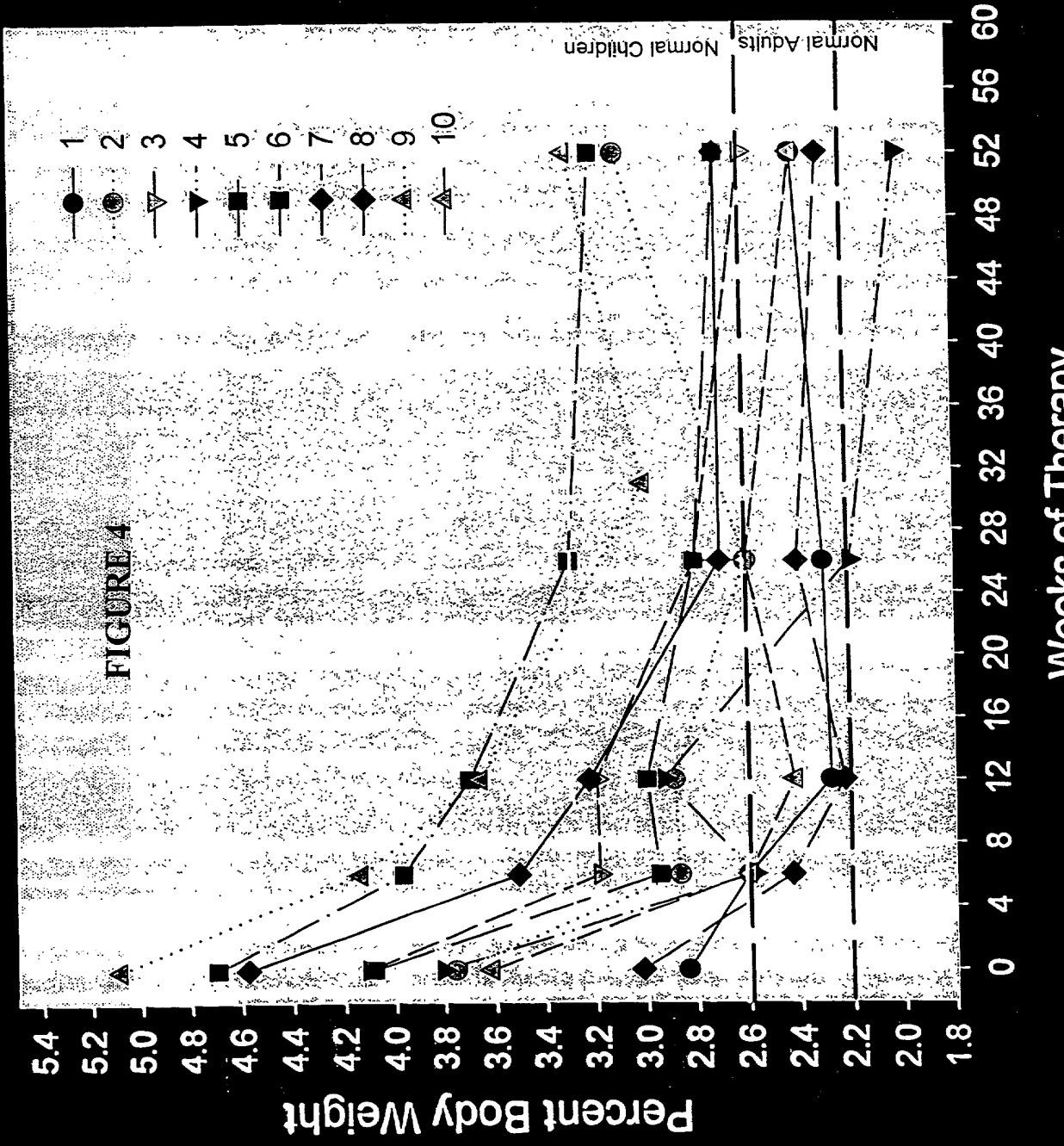


FIGURE 4

Urinary GAG Excretion During Enzyme Therapy

FIGURES

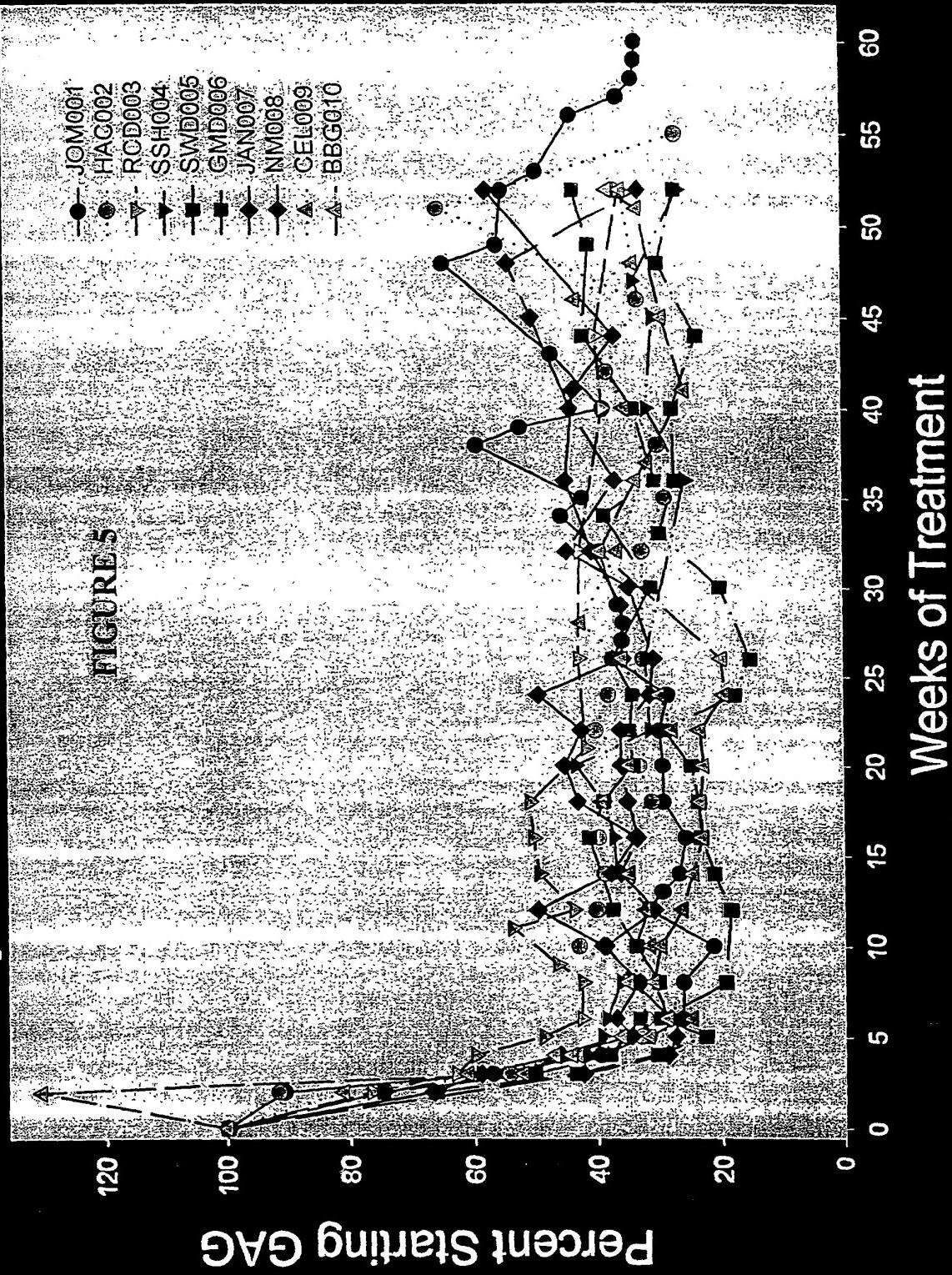


FIGURE 5

Elbow and Knee Extension in HAC_{0.02}

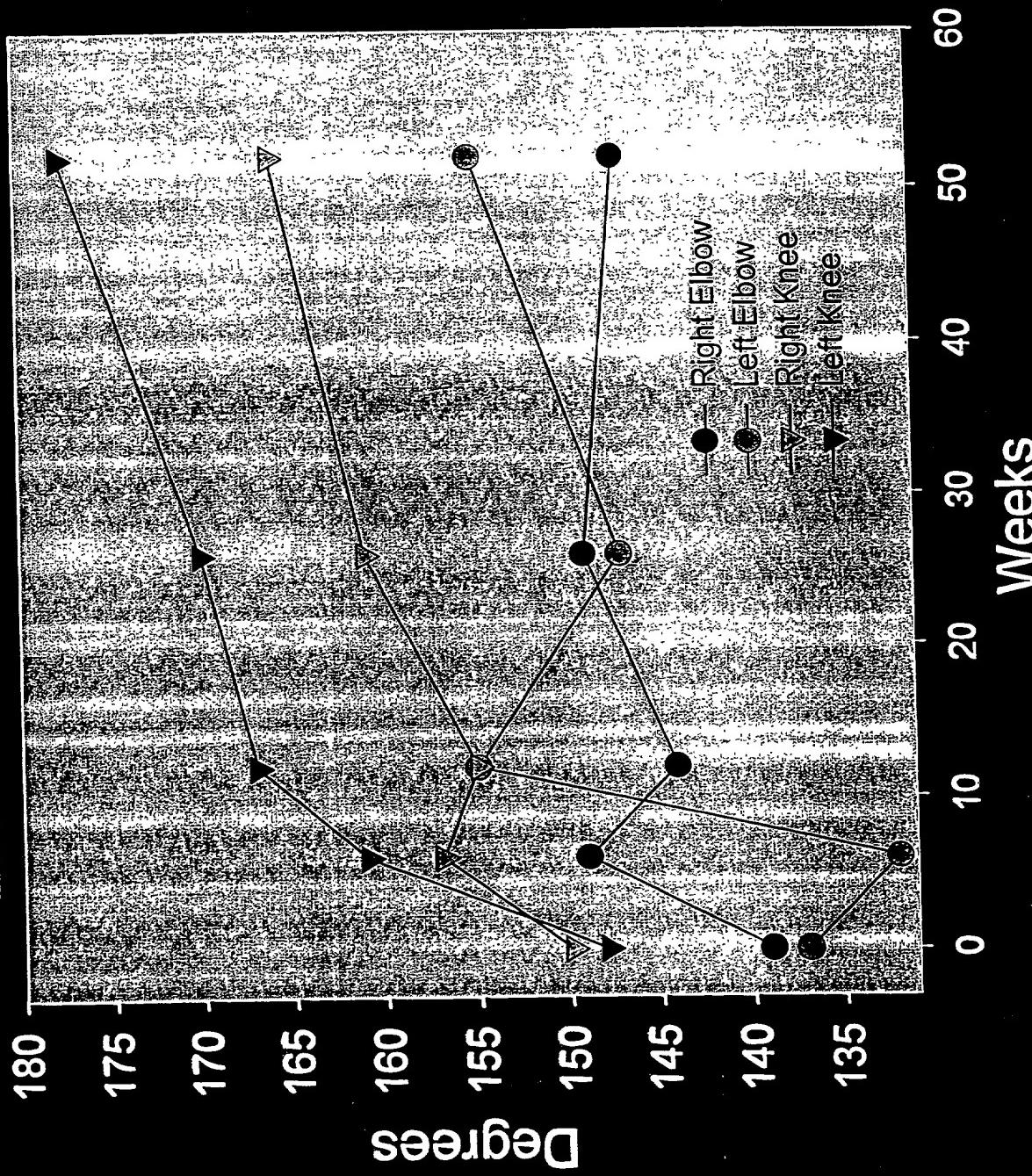


FIGURE 6

Surgeon's view of just restriction
four patients

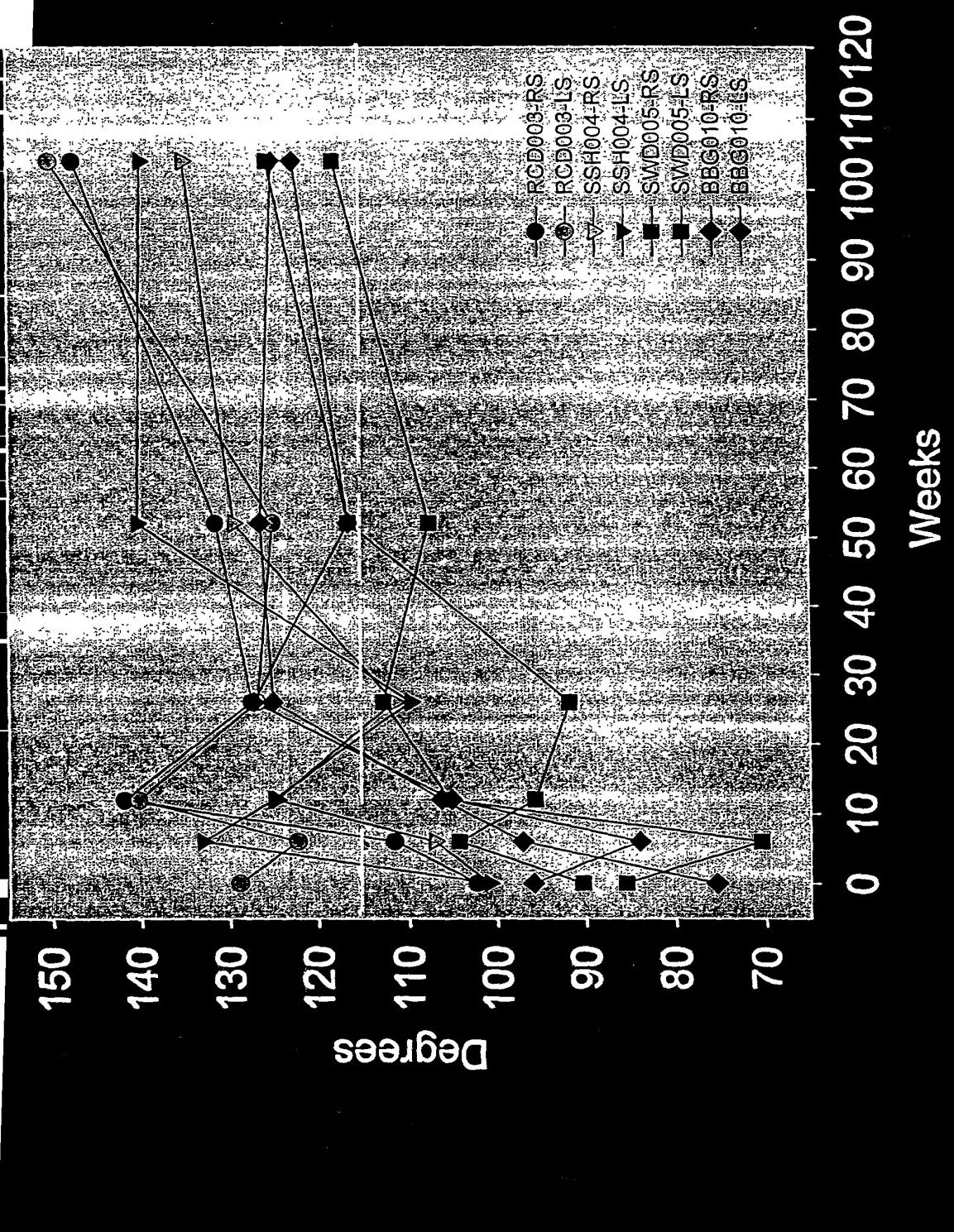


FIGURE 7

Sleep Apnea improves

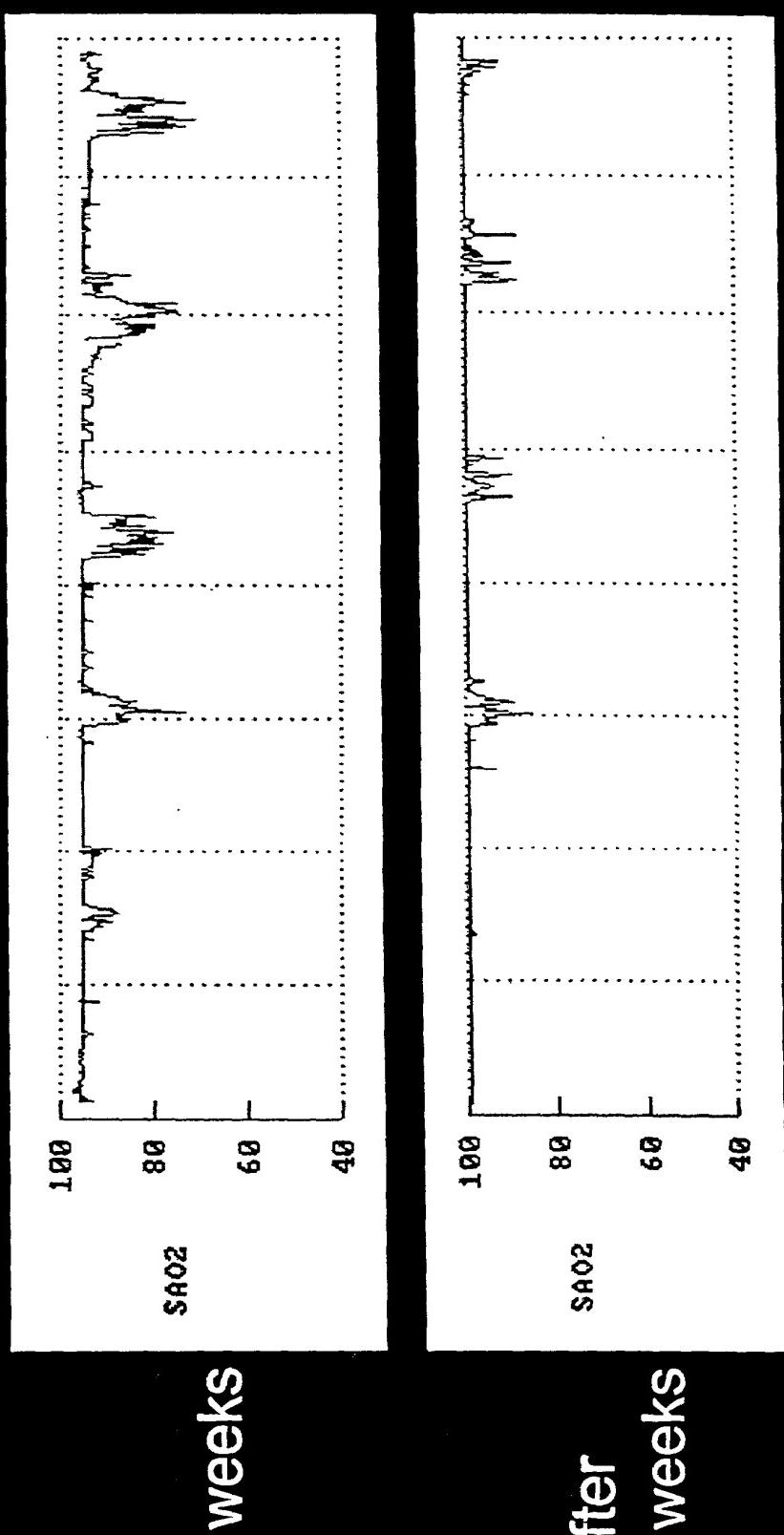


FIGURE 8

Apneas + Hypopneas During Sleep Pre and Post Treatment

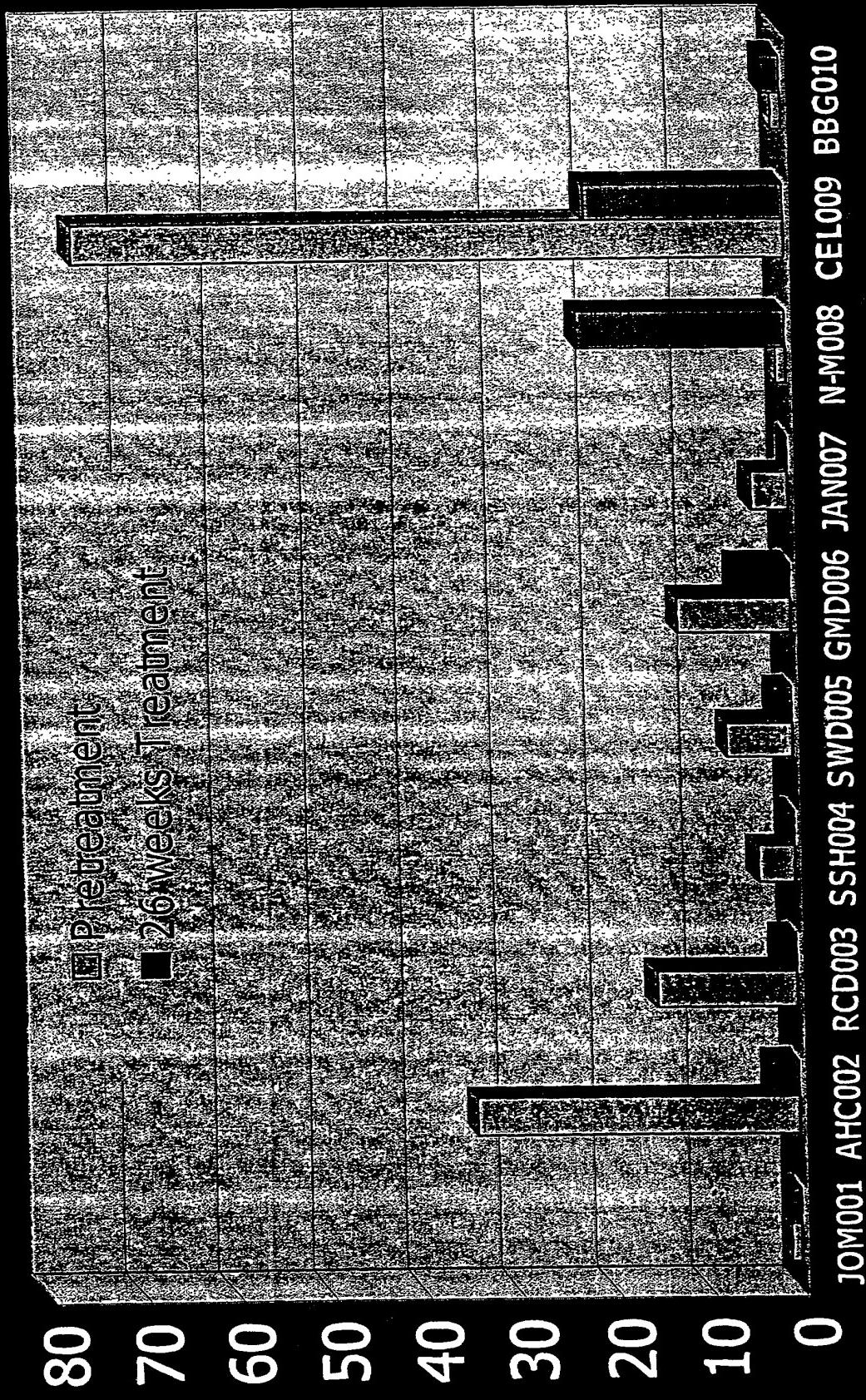


FIGURE 9

JOM001 AHC002 RCD003 SSH004 SWD005 GMD006 JAN007 N-M008 CEL009 BBG010

Pulmonary Function Tests in GVID 006

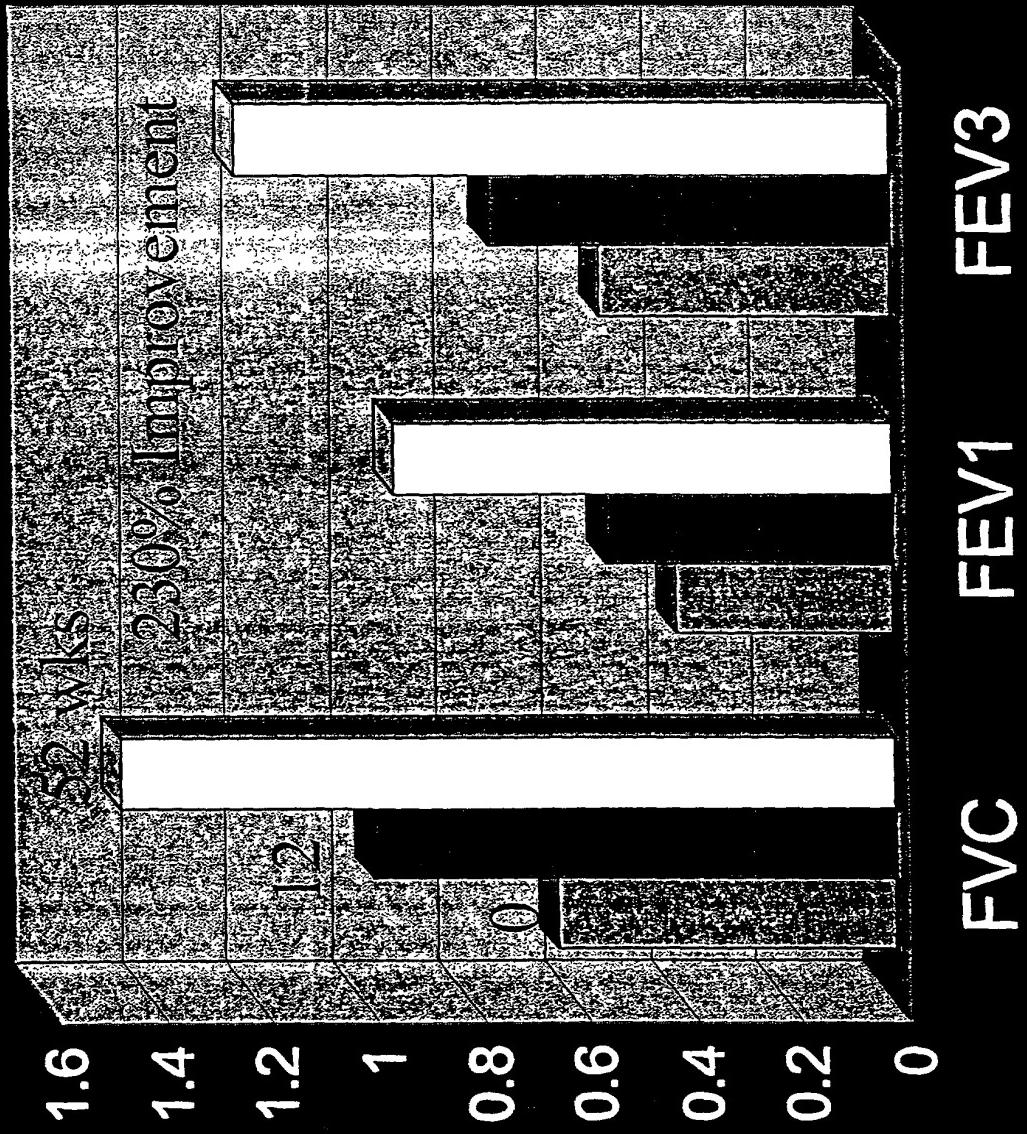


FIGURE 10

Increased Height Growth Velocity

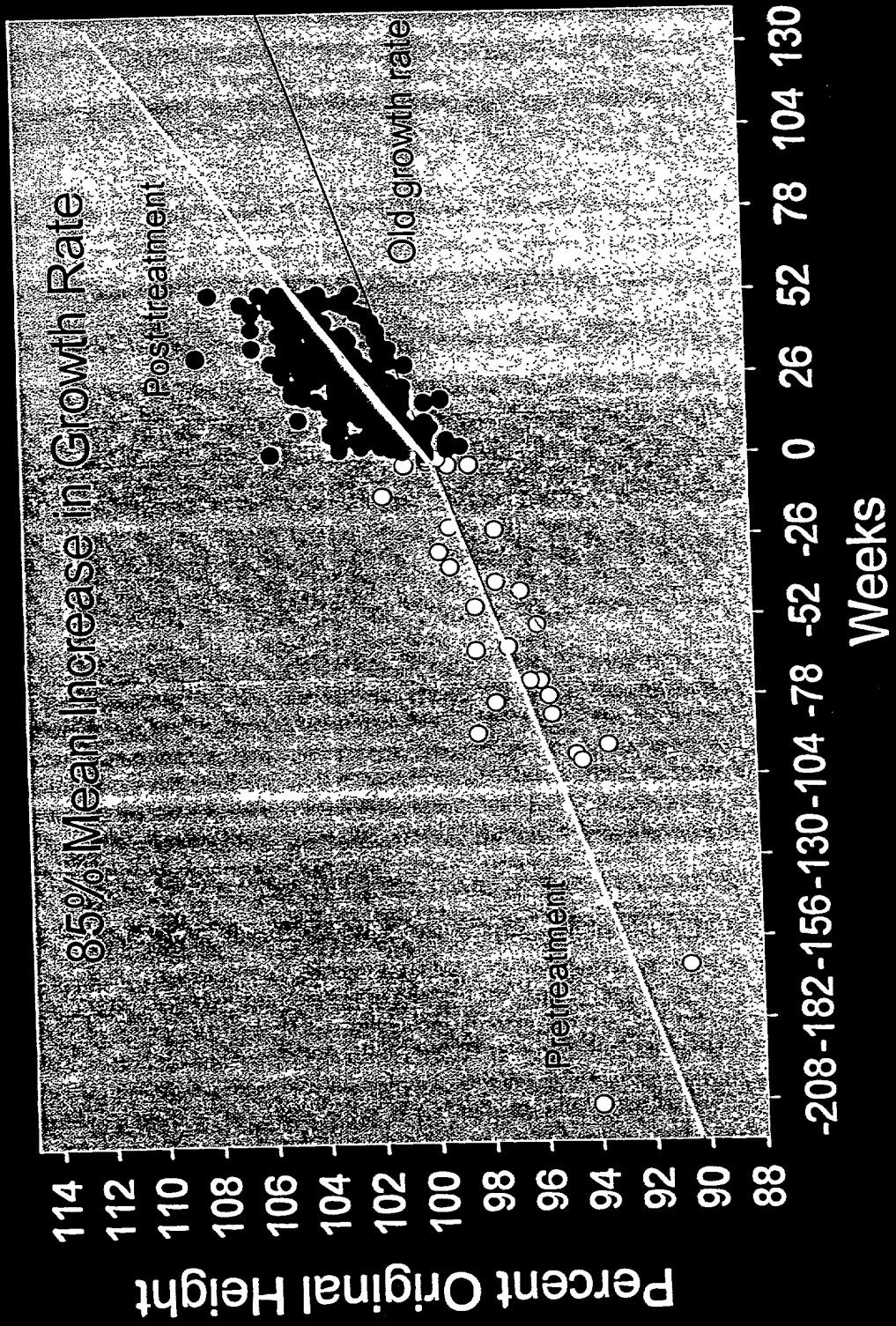


FIGURE 11

FIGURE 12.

COMPARISON OF HOST PROTEIN CONTAMINATION BETWEEN A PRIOR AND THE NEW GALLI PROCESS

Chinese Hamster Ovary Host Protein Contamination by ELISA Assay

SOURCE AND BATCH NUMBER	CHOP PROTEIN CONTAMINATION (microgram per milligram)	PERCENT CHOP CONTAMINATION	PURITY OF THE ENZYME FROM CHOP
Prior Process (Carson/REI)			
C9002	14	1.4%	98.6%
C9003	24	2.4%	97.6%
C9004	16	1.6%	98.4%
New Process (Galli)			
P1003	<1.3	<0.13%	>99.9%
P1006	1.2	0.12%	99.9%
P1007	<0.6	<0.06%	>99.9%
P1008	<0.67	<0.067%	>99.9%

FIGURE 12

Comparison of Galli and Carson Material

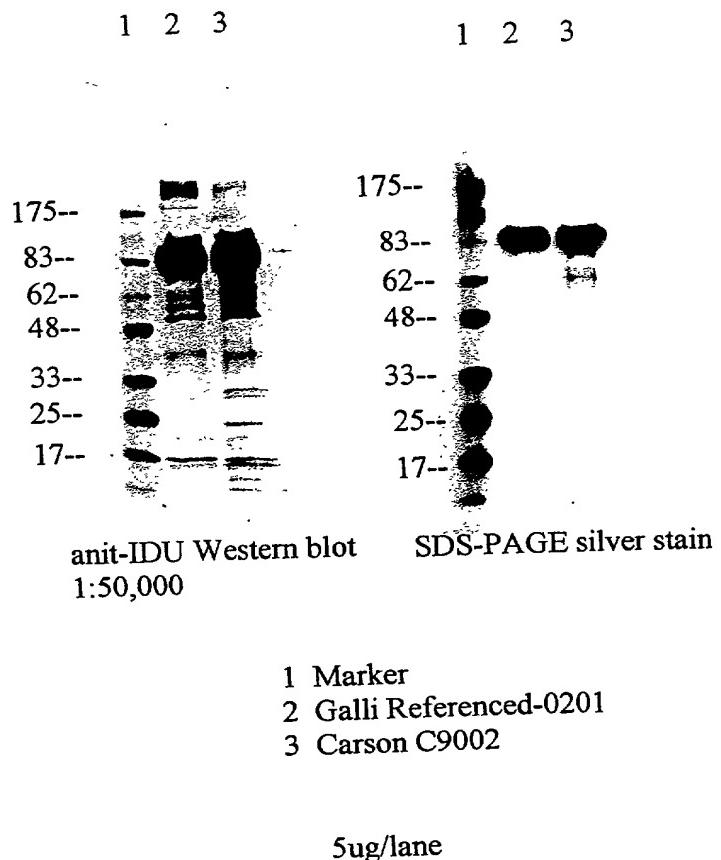


FIGURE 13